

LOCUS AF089816 1765 bp mRNA linear PRI 24-OCT-1998  
 DEFINITION Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.  
 ACCESSION AF089816  
 VERSION AF089816.1 GI:3789933  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1765)  
 AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.  
 TITLE GIPC, a PDZ domain containing protein, interacts specifically with  
 the C terminus of RGS-GAIP  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12340-12345 (1998)  
 MEDLINE 98445373  
 PUBMED 9770488  
 REFERENCE 2 (bases 1 to 1765)  
 AUTHORS De Vries,L., Lou,X., Zhao,G., Zheng,B. and Farquhar,M.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-SEP-1998) CMM, UCSD, 9500 Gilman Drive, La Jolla, CA  
 92093, USA  
 FEATURES Location/Qualifiers  
 source 1. .1765  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="GC"  
 /tissue\_type="pituitary"  
 /note="growth hormone secreting cells"  
 CDS 88. .1089  
 /codon\_start=1  
 /product="RGS-GAIP interacting protein GIPC"  
 /protein\_id="AAC67548.1"  
 /db\_xref="GI:3789934"  
 /translation="MPLGLGRRKKAPPLVENEAEAPGRGGLGVGEPGPLGGGSGGPQ  
 MGLPPPPPALRPRLVFHTQLAHGSPTGRIEGFTNVKELYGKIAEAFRLPTAEVMFCTL  
 NTHKVDMDKLLGGQIGLEDFIFAHVKGQRKEVEVFKSEDALGLTITDNGAGYAFIKRI  
 KEGSVIDHIHLISVGDMEIAINGQSLGCRHYEVARLLKELPRGRTFTLKLTEPRKAF  
 DMISQRSAGGRPGSGPQLGTGRGTLRLRSRGPATVEDLPSAFEKAIEKVDDLLESYM  
 GIRDTELAATMVELGDKRNPDELAELDERLGDFAFPDEFVFDVWGAIGDAKVGRY"  
 misc\_feature 460. .762  
 /note="encodes PDZ domain"  
 misc\_feature 877. .1047  
 /note="encodes ACP domain"  
 BASE COUNT 332 a 561 c 568 g 304 t  
 ORIGIN

Alignment Scores:

Pred. No.:	2.08e-102	Length:	1765
Score:	1713.00	Matches:	330
Percent Similarity:	99.10%	Conservative:	0
Best Local Similarity:	99.10%	Mismatches:	3
Query Match:	99.59%	Indels:	0
DB:	9	Gaps:	0

US-10-013-056-2 (1-333) x AF089816 (1-1765)

Qy	1	MetProLeuGlyLeuGlyArgArgLysLysAlaProProLeuValGluAsnGluGluAla	20
Db	88	ATGCCGCTGGGACTGGGGCGCCGAAAAAGGCGCCCCCTCTAGTGGAATGAGGAGGCT	147
Qy	21	GluProGlyArgGlyGlyLeuGlyValGlyGluProGlyProLeuGlyGlyGlySer	40
Db	148	GAGCCAGGCCGTGGAGGGCTGGGCGTGGGGGAGCCAGGGCCTTTGGGCGGAGGTGGGTTCG	207
Qy	41	Gly***ProGlnMetGly*****ProProProProAlaLeuArgProArgLeuValPhe	60
Db	208	GGGGGCCCCCAAATGGGCTTGCCCCCCCCCTCCCCAGCCCTGCGGCCCCGCTTGTGTTC	267
Qy	61	HisThrGlnLeuAlaHisGlySerProThrGlyArgIleGluGlyPheThrAsnValLys	80
Db	268	CACACCCAGCTGGCCCATGGCAGTCCCACTGGCCGCATCGAGGGGTTACCAACGTCAAG	327
Qy	81	GluLeuTyrGlyLysIleAlaGluAlaPheArgLeuProThrAlaGluValMetPheCys	100
Db	328	GAGCTGTATGGCAAGATTGCCGAGGCCTTCCGCCTGCCAACTGCCGAGGTGATGTTTTGC	387
Qy	101	ThrLeuAsnThrHisLysValAspMetAspLysLeuLeuGlyGlyGlnIleGlyLeuGlu	120
Db	388	ACCTGAACACCCACAAAGTGGACATGGACAAGCTCCTGGGGGGCCAAATCGGGCTGGAG	447
Qy	121	AspPheIlePheAlaHisValLysGlyGlnArgLysGluValGluValPheLysSerGlu	140
Db	448	GACTTCATCTTCGCCCACGTGAAGGGGCAGCGCAAGGAGGTGGAGGTGTTCAAGTCGGAG	507
Qy	141	AspAlaLeuGlyLeuThrIleThrAspAsnGlyAlaGlyTyrAlaPheIleLysArgIle	160
Db	508	GATGCACTCGGGCTCACCATCACGGACAACGGGGCTGGCTACGCCTTCATCAAGCGCATC	567
Qy	161	LysGluGlySerValIleAspHisIleHisLeuIleSerValGlyAspMetIleGluAla	180
Db	568	AAGGAGGGCAGCGTGATCGACCACATCCACCTCATCAGCGTGGGCGACATGATCGAGGCC	627
Qy	181	IleAsnGlyGlnSerLeuLeuGlyCysArgHisTyrGluValAlaArgLeuLeuLysGlu	200
Db	628	ATTAACGGGCAGAGCCTGCTGGGCTGCCGGCACTACGAAGTGGCCCGGCTGCTCAAGGAA	687
Qy	201	LeuProArgGlyArgThrPheThrLeuLysLeuThrGluProArgLysAlaPheAspMet	220
Db	688	CTGCCCCGAGGCCGTACCTTCACGCTGAAGCTCACGGAGCCTCGCAAGGCCTTCGACATG	747
Qy	221	IleSerGlnArgSerAlaGlyGlyArgProGlySerGlyProGlnLeuGlyThrGlyArg	240
Db	748	ATCAGCCAGCGTTTCAGCGGGTGGCCGCCCTGGCTCTGGCCCACTGGGCACTGGCCGA	807
Qy	241	GlyThrLeuArgLeuArgSerArgGlyProAlaThrValGluAspLeuProSerAlaPhe	260
Db	808	GGGACCCTGCGGCTCCGATCCCGGGGCCCCGCCACGGTGGAGGATCTGCCCTCTGCCTTT	867
Qy	261	GluGluLysAlaIleGluLysValAspAspLeuLeuGluSerTyrMetGlyIleArgAsp	280
Db	868	GAAGAGAAGGCCATTGAGAAGGTGGATGACCTGCTGGAGAGTTACATGGGTATCAGGGAC	927
Qy	281	ThrGluLeuAlaAlaThrMetValGluLeuGlyLysAspLysArgAsnProAspGluLeu	300

Db	928	ACGGAGCTGGCGGCCACCATGGTGGAGCTGGGAAAGGACAAAAGGAACCCGGATGAGCTG	987
Qy	301	AlaGluAlaLeuAspGluArgLeuGlyAspPheAlaPheProAspGluPheValPheAsp	320
Db	988	GCCGAGGCCCTGGACGAACGGCTGGGTGACTTTGCCTTCCCTGACGAGTTCGTCTTTGAC	1047
Qy	321	ValTrpGlyAlaIleGlyAspAlaLysValGlyArgTyr	333
Db	1048	GTCTGGGGCGCCATTGGGGACGCCAAGGTCGGCCGCTAC	1086